1 Docket No. GIO-001.01

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3 # SYSTEMS AND METHODS FOR SEQUENCE COMPARISON

4

5 ## ABSTRACT

6 **[0057]** Methods and systems for comparing a first sequence and a second sequence,

7 including associating errors with alignments of the first sequence and the second sequence,

8 comparing the alignment errors to identify the alignment having the smallest error, and, based on

9 the alignment having the smallest error, computing: a first percent identity relative to the first

10 sequence, and a second percent identity relative to the second sequence.